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Sequence 4645, Ap
Sequence 31294, Ap
Sequence 31294, A
Sequence 5207, Ap
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Sequence 12639, Ap
Sequence 12639, Ap
Sequence 3876, Ap
Sequence 3876, Ap
Sequence 1046, Ap
Sequence 1046, Ap
Sequence 1046, Ap
Sequence 248, Appl
Sequence 3448, Ap
Sequence 248, Appl
Sequence 7451, Appl
Sequence 228, Appl
Sequence 288, Appl
                                                                                                                                        April 22, 2005, 16:19:29 ; Search time 29.9558 Seconds (without alignments) 844.779 Million cell updates/sec
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1740
1 MCAQYCISFADVEKAHINIQ......TSLNWVGQAERPAPYQTVSV 339
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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S-09-902-540-12639
IS-09-543-681A-4364
S-09-552-991A-22442
IS-09-134-001C-3876
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-09-489-039A-14107
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5-09-328-352-7451
5-09-107-433-2928
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-08-403-866-10
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nnunnnunnunnundanna a oo zzmaalzoo a a oo	S-09-949-016-10697 Sequence 10697, A S-09-088 435-1 Sequence 1, Appli Scotland Color	ALIGNMENTS	A. 6458576el Human Pyridoxal-Phosphate 5nzyme Family Member and Uses Therefore 9/789,300A 183,208	Score 1582.5; DB 4; Length 340; Pred. No. 1.6e-165; 9; Mismatches 15; Indels 1; Gaps 1;	MCAQYCISFADVEKAHINIODSIHLTPVLJSSILNQIAGRNLFFKCELFQKTGSFKIRGA 60 	LNAIRGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQA 120 	YGASIVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGGGTIALEVLNQVPLVDAL 180 	VVPVGGGGNVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGV 240		339
28 261.5 29 254.5 31 252.5 31 252.5 31 252.5 32 242.5 33 229.5 34 20.5 35 205.5 36 205.5 36 205.5 37 204.5 38 205.5 39 196 44 185.5 44 185.5 44 185.5 44 185.5 44 185.5 44 185.5 44 185.5 44 185.5 44 185.5 44 185.5 44 185.5 44 185.5 44 185.5 44 185.5 44 186.5 50FURANT MACHARIT APPLICANT APPLICAN	.6 325 3 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		lication US/097893 FITON: ers, Rachel ers, Rachel ers, Rachel HIDON: 22406, A NO. TION: Dependent E: 35800/208926 FITON: DEPENDENT US/05/100 NUMBER: US/06/05/100 NUMBER: US/07/100 NUMBER: US/07/100 NUMBER: US/07/100 NUMBER: US/05/100 NUMBER: US/0	Ä	QYCISFADVEKAHINIQD 	IRGLIPDTPEEKPKAVVT 	SIVYCDPSDESREKVTQR      :          SIVYCEPSDESRENVAKR	VGGGGMVAGIAITĪKALK                 VGGGGMLAGIAITVKALK	I.GLNTWPIIRDLVDDVFT	BVKNVCIVLSGGNVDLT-     :         BVKNICIVLSGGNVDLTS
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Sequence 31294, Application US/09252991A
Patent No. 6551795
Patent No. 6551795
Patent No. 6551795
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO FSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/74,788
PRIOR APPLICATION NUMBER: US 60/74,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-7
NUMBER: OS 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: OS 60/094,190
                                                                                                                       68 IPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVY 127
                                                                                                                                                                                             128 CDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGG 187
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68 IPDTPEEKEKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVY 127
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31.2%; Score 543; DB 4; Length 37
Best Local Similarity 38.7%; Pred. No. 6.9e-51;
Matches 121; Conservative 63; Mismatches 121; Indels
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US-09-252-991A-31294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 -KNVCIVLSGGNVDLT 320
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US-09-252-991A-31294
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                                                    Sequence 4645, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/543,681A
PRIOR APPLICATION NUMBER: US 60/128,706
RICHE APPLICATION NUMBER: US 60/128,706
RICHE FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
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Sequence 4536, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BADWANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PILLING DATE: 1999-0328,352
CURRENT FILING DATE: 1999-06-04
SEQ ID NOS: 8252
LENGER OF SEQ ID NOS: 8252
LENGER OF SEQ ID NOS: 8252
LENGER OF SEG ID NOS: 8252
LENGER OF SEG ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 GMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETJADGVKSS-IGL 246
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Pred. No. 6.5e-58;
9; Mismatches 108; Indels
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Best Local Similarity 40.8%; Pred. No. 2.7e-54;
Matches 129; Conservative 62; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

Best Local Similarity 40.9%; Pre
Matches 128; Conservative 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Proteus mirabilis
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310 KIGIIISGGNVDI 322
                                US-09-543-681A-4645
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US-09-328-352-4536
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Sequence 5207, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTO9-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                          of amino acid at the above locations are unknown
                                                                                                                                                                                                                                                                                                 86 NHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGA-SIVYCDPSDESREKVTQRIMQ 144
                                                                                                                                                                                                                                                                                                                           98 NHAQGLALAAAXRQGIRAVIVMPKTTPEIKVQAVRAHGAKAVLHGDAFPEALAHAL-KLVD 156
                                                                                                                                                                                                                                                                                                                                                                                                                              263 TEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEVKNVCIVLSGGNVDLTSL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 AGIAITIKALKPSVKVYAAE----PSNADDCYQSKLKGELTPNLHPPETIADGVK-SSIG 245
                                                                                                                                                                                                                                                                                                                                                                                                 145 ETEGILVHPNQEPAVIAGQGTIALEVLNQVP-LVDALVVPVGGGGMVAGIAITIKALKPS 203
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                                                                                                                                                                                                                                               41 TPLQPARQLSERLGNQVLLKREDLQPVFSFKIRGAYNKVAQL---TEEEKARGVIAASAG 97
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                                                                                             ; Score 457.5; DB 4; Length 524; ; Pred. No. 3.2e-41; 58; Mismatches 123; Indels 11;
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25.9%; Score 450.5; DB 4; Length
Best Local Similarity 34.5%; Pred. No. 1.3e-40;
Matches 109; Conservative 57; Mismatches 127; Indele
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US-09-328-352-5207
                                                                                             Query Match 26.3%;
Best Local Similarity 37.7%;
Matches 116; Conservative 5
                       ; OTHER INFORMATION: Identity US-09-252-991A-27783
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US-09-328-352-5207
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LOCATION:
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GENERAL INFORMATION:

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GENERAL INFORMATION:

APPLICATION:

APPLICATION:

TITLE OF INVENTION:

ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27783

LENGTH: 524
                                                                                                                                                                    APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 L---TAAEKRKGVVACSAGNHAQGVSLSCAMLGIDGKVVMPKGAPKGAPKSKVAATCDYSAEVV 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 LHGDNFNDTLAKASDIV--ELEGRIFIPPYDDPQVIAGGGTIGLEILEDLYDVDNVIVPI 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 PGKLTYEIARQLVDDIVLVSEDDIRQSMVALIQRNKVITEGAGALACAALLSGKLDSYIQ 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 27.6%; Score 480; DB 4; Best Local Similarity 36.3%; Pred. No. 5e-44; Matches 117; Conservative 66; Mismatches 129
                                                                                                                                                                                                                                          FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
SEQ ID NOO 14107
                                                                                     Sequence 14107, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14107
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                                                                        US-09-489-039A-14107
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Sequence 22442, Application US/09252991A
Patent No. 651795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AEXCIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 VAVKRIGDETFRLCQKYVDDVITVDSDAICAAVKDLFEDVRAIAEPSGALALAG-LKKYV 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261
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                                                                                                                                                                                                                                                                                                                                                                        125 IVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGOGTIALEVLNQVPLVDALVVPV
                                                                                                                                                                                                    8 SFADVEKAHIN--IQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIR
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                                                                                                                                                         66; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.4%; Score 406.5; DB 4;
33.0%; Pred. No. 2.1e-35;
live 62; Mismatches 132;
                                                                                                                Score 418; DB 4;
Pred. No. 7.3e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 EEHQIKGERLAHVLSGANVNFHGLRYVSE 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 QTVSPEVKNVCIVLSGGNVDLTSLNWVGQ 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62;
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                                                                                                         24.0%;
                                                 ORGANISM: Proteus mirabilis
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SEQ ID NO 22442
                                                                                                                                                       Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 109; Conservative
                                                                                                                                  Best Local Similarity
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US-09-252-991A-22442
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                                                                 US-09-543-681A-4364
      LENGTH: 525
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                                                                                                                Query Match
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Batent No. 6605709

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: GARY BEETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 1999-04-09

PRIOR PELLING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344
      299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 GGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVK-SS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 IVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 IGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKULIEPTAGVALAAVLSQHFQTVSP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                     APPLICANT: Goldman, Barry S.
APPLICANT: Glodman, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Steven C.
APPLICANT: Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REPRENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR PLING DATE: 2000-07-10
RUMBER OF SEQ ID NOS: 16825
SEQ ID NO 12639
LENGTH: 405
ELTTQIAKHFVDDIVVVTEDMIEEAIALLINIEKTVCEGAGATGIAAIMSR-----PDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 ISFADVEKAHINIQDSIHLTPVLTSSILNQ-IAGRNLFFKCELFQKTGSFKIRGALNAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.9%; Score 434; DB 4; 32.8%; Pred. No. 8.1e-39;
                                                                                                                                                                                        Sequence 12639, Application US/09902540 Patent No. 6833447
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297 RGRRTAILLSGGNIDMNVIS 316
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                                          ---KNVCIVLSGGNVD 318
                                                               300 FLGHKVGVVLSGGNID 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Myxococcus xanthus US-09-902-540-12639
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Best Local Similarity 32.8*
Matches 105; Conservative
                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                         US-09-902-540-12639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 --IVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQV----PLVD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 EIVLIGDTFDHCLAQALNYTKOHKMN-FIDPFNNVYTIAGOGTLAKEILNOAEKEDKTFD 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 LIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGAS-- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 ALVVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIAD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 GVK-SSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQH 297
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3-8040S
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN VET: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 21.0%; Score 365; DB 3; Length 424; Best Local Similarity 29.8%; Pred. No. 3.5e-31; Matches 97; Conservative 60; Mismatches 152; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 KKQI--ENKTIVCIVSGGNNDINRM 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 FQTVSPEVKNVCIVLSGGNVDLTSL 322
                                             60/055,779
                                                                                                                                                                                                                                                                                 , ORGANISM: Staphylococcus epidermidis US-09-134-001C-3876
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ORGANISM: Artificial Sequence
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3876
LENGTH: 424
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US-09-710-279-1046
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LENGTH: 424
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Sequence 3876, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF I
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FILE REFERENCE: 2709.2004001.
CURRENT APPLICATION NUMBER: US/09/489,039A
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PRIOR PLILING DATE: 1999-01-29
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369 DIRVIGVEPEDS-NCLQAALAAGERVVLGQVGLFADGVAVAQIGACNFEVCKDHVDEVIT 427
                                                                                                                        VTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEVKNVCIVLSGGNVDLTS 321
                                                                                                                                                                     265 YLDDIITVDSDAICAAMKDLFEDVRAVAEPSGALALAGMKKYIAQH----NIRGERLAHI 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 VVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVYCDPS-DESREK 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 KOLMPOIKVIAVE---AEDSACLKAALDAGHPVDLPRVGLFAEGVAVKRIGDETFRLCOE 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 KALKPSVKVYAAEPSNADD--CYQSKLKGELTPNLHPPETIADGVK-SSIGLNTWPIIRD 254
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32 VYEAVQKTPLQKMDKLSSRLDNVILVKREDRQPVHSFKLRGAYAMMSSL---TAEQKSHG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 IQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGLIPDTPEEKPKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Gaps
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                                                                                                                                                                                                                                                                                                                                       322 LNWVGQ-----AERPAPYQ 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8050, Application US/09489039A
Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 LSGANVNFHGLRYVSE 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312 LSGGNVDLTSLNWVGQ 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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US-09-134-001C-3876
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315 AIISGANMNFDRLRYI--AER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: M.catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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--IVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQV----PLVD 178
                                                                                                                     179 ALVVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIAD 238
                                             126 EIVLIGDTFDHCLAQALNYTKQHKMN-FIDPFNNVYTIAGQGTLAKEILNQAEKEDKTFD 184
                                                                                                                                                               : :||||:::|:: || | | : | || : | || : | || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
                                                                                                                                                                                                                                             239 GVK-SSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQH 297
                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 KAHINIQDSIHLIPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGLIPDTPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ehrlich, Stanislav
APPLICANT: Ehrlich, Stanislav
APPLICANT: Godon, Jean-Jacques
APPLICANT: Renault, Pierre
TITLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate
TITLE OF INVENTION: Synthase from Lactococcus and its applications
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPALIZACION COPERATING SYSTEM: PC-DOS/MS-DOS COPTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

20.7%; Score 359.5; DB 1;
Best Local Similarity 29.4%; Pred. No. 1.5e-30;
Matches 98; Conservative 67; Mismatches 145;
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                                                                                                                                                                                                                                                                                                                                                                  298 FQTVSPEVKNVCIVLSGGNVDLTSL 322
                                                                                                                                                                                                                                                                                                                                                                                                      304 KKQI--ENKTIVCIVSGGNNDINRM 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GOLDMAN, MICHAEL I.
RESISTRATION NUMBER: 30, 727
REFERENCE/DOCKET NUMBER: 20747/30
TELECHONE: (716) 263-1600
TELEFAX: (716) 263-1487
TELEFAX: (716) 263-1487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/08403866
Patent No. 5643779
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   441 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-403-866-10
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Sequence 3648, Application US/09540236
Fatent No. 6673910
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARF
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 3548
186 GGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVK-SSI 244
                                           210 GGGLIAGITAYSKERYPQTEIIGVEAKGATSMKAAYSAGQ-PVTLEHIDKFADGIAVATV 268
                                                                                         245 GLNTWPIIRDLVDDVFTVTEDBIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPE 304
                                                                                                                     10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 RIMQETEGI-LVHPNQEPAVIAGOGTIALEVLNQVPLVDALVVPVGGGGKVAGIAITIKA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 K--AETDGMTYIAPYDDELVIAGOGTIGLELTQOWRNIDYVFIACGGGGLLAGVAAFLGE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 ----DLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEVKNVC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 GSGTVIEPEIVTCTNDEICAAIKDIFEENRSIVE-TAGALSVAGMKKFIQTHNLSGKNCV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 SIHLTPVLTSSILNQIAGRNLFFKCELFOKTGSFKIRGALNAIRGLIPDTPEEKPKAVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 LKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVK-SSIGLNTWPIIR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.4%; Score 355; DB 4; Length 518; 31.2%; Pred. No. 6.2e-30; tive 66; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                             305 V--KNVCIVLSGGNVDLTSLNWVGQAERPAPYQ 335
                                                                                                                                                                                                               324 IKGKNIVCIISGGNNDISRRQEI--EERALVYE 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: April 22, 2005, 16:26:54 Job time : 31.9558 secs
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Sequence Sequence

Sequence 3857, A Sequence 39197, A Sequence 39197, A Sequence 27, Appl Sequence 12, Appl Sequence 12, Appl Sequence 20, Appl Sequence 4, Appl Sequence 67, Appl Sequence 67, Appl Sequence 63, Appl Sequence 59, Appl Sequence 59, Appl Sequence 26, Appl Sequence 26, Appl Sequence 26, Appl Sequence 276, Appl Sequence 4591, Appl Sequence 3828, Appl Sequence 37804, Appl Sequence 670, Appl Sequence

S US-10-413-943-31
S US-10-424-599-266101
S US-10-425-114-38570
S US-10-425-114-38570
S US-10-425-114-38197
S US-10-425-114-38197
S US-10-413-943-27
S US-10-413-943-12
S US-10-413-943-12
S US-10-413-943-64
S US-10-413-943-67
S US-09-738-626-5828
US-09-738-626-5828
US-09-738-626-673
S US-10-287-226-673
S US-10-287-226-673
S US-10-287-226-673
S US-10-287-226-673
S US-10-377-072-17

10040 10040 10040 10060 10

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US-09-789-300A-2
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LENGTH: 340
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375
374.5
373.5
371.5
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336.5
336.5
336.5
296.5
296.5
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April 22, 2005, 16:23:43 ; Search time 88.3697 Seconds (without alignments) 1276.639 Million cell updates/sec
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                                                                                                                                                                                                   1 MCAQYCISFADVEKAHINIQ.....TSLNWVGQAERPAPYQTVSV 339
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| cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBGOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBGOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US09_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
             GenCore version 5.1.6
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4 US-10-164-966-2

5 US-10-240-860-2

5 US-10-240-466-2

5 US-10-240-466-2

5 US-10-240-466-2

5 US-10-264-237-2089

5 US-10-437-963-106995

5 US-10-425-114-62567

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US-10-424-599-155063

US-10-156-761-10839

US-10-156-761-10839

US-10-413-943-33
                                                                                                                                                                                                                                                                                                                  of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                  1424015 seqs, 332791073 residues
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                                                                          OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1740
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Match
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1582.5
1582.5
1578.5
756.5
640.5
640.5
485.5
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                                                                                                                                                                                                        Sequence:
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Sequence 17, Appl Sequence 17, Appl Sequence 2128, Ap Sequence 164, App

ALIGNMENTS

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YGASIVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDAL 180
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US-09-789-300A-2
US-09-789-300A-2
US-09-789-300A-2
Sequence 2, Application US/09789300A
Publication No. US20020115137A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 22406, A No. 6458576e1 Human Pyridoxal-Phosphate
TITLE OF INVENTION: Dependent Enzyme Family Member and Uses Therefore
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                                                                                                                                                                                                                                                                                                                                                                                                                                              90.9%; Score 1582.5; DB 9; 89.7%; Pred. No. 3.7e-146; Live 19; Mismatches 15;
                                                                                                                                                                    FILE REFERENCE: 35800/208926
CURRENT APPLICATION NUMBER: US/09/789,300A
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: US 60/183,208
PRIOR FILING DATE: 2000-02-17
                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local S
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Sequence 2, Appli Sequence 2, Appli Sequence 2089, Ap Sequence 2089, Ap Sequence 49567, A Sequence 49567, A Sequence 43761, A Sequence 43071, A Sequence 43071, A

200.09 20

Sequence 2, Appli

Sequence 33, Appl Sequence 29, Appl

120

180

240

us-09-889-609b-8.rapb

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61 LNAIRGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQA 120
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Sequence 2, Application US/10240800

Publication No. US20030212262A1

GENERAL INFORMATION:

TITLE OF INVENTION: HUMAN SERINE RACEMASE

FILE REFERENCE: 20642Y-PCT:

CURRENT APPLICATION NUMBER: US/10/240,800

CURRENT PILING DATE: 2002-10-03

PRIOR FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 8

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FASELSEQ FOR Windows Version 4.0
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US-10-240-800-2
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TYPE: PRT
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APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Radiolph-Owen, Laura A.
ITILE OF INVENTION: Novel Nucleic Acid Sequences Encoding Melanoma
ITILE DE INVENTION: Novel Nucleic Acid Sequences Encoding Melanoma
ITILE DE INVENTION: Novel Nucleic Acid Sequences Encoding Melanoma
ITILE DE INVENTION: Molecules, Arpaes Molecules, Aminotransferase
ITILE DE INVENTION: Pyridoxal-Phosphace Dependant Enzyme Molecules,
ITILE DE INVENTION: Pyridoxal-Phosphace Dependant Enzyme Molecules
ITILE DE INVENTION: Pyridoxal-Phosphace Dependant Enzyme Molecules
ITILE DE INVENTION: Pyridoxal-Phosphace Dependant Enzyme Molecules
ITILE DE INVENTION: Dyridoxal-Phosphace Dependant Enzyme Molecules
ITILE REPERBANCE: 3060-0744760
CURRENT FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR PELICATION NUMBER: 60/250, 948
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-07-99
PRIOR PELICATION NUMBER: 60/219, 740
PRIOR PELICATION NUMBER: 60/219, 740
PRIOR PELICATION NUMBER: 60/219, 740
PRIOR PELICATION NUMBER: 60/214, 138
PRIOR PELICATION NUMBER: 60/219, 300
PRIOR PELICATION NUMBER: 60/219, 30
121 YGASIVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDAL 180
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                                               VVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGV
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90.9%; Score 1582.5; DB 14; Length 340;
Best Local Similarity 89.7%; Pred. No. 3.7e-146;
Matches 305; Conservative 19; Mismatches 15; Indels 1;
                                                                                                                                                                                                                         301 VSPEVKNVCIVLSGGNVDLT-SLNWVGQAERPAPYQTVSV 339
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Publication No. US20030064439A1
GENERAL INFORMATION:
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APPLICANT: Glucksmann Maria
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TYPE: PRT
ORGANISM: Homo sapiens
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US-10-437-963-106995
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APPLICANT:
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        JOS-10-240-466-2

Sequence 2, Application US/10240466

Bedication No. US20030175941A1

GENERAL INFORMATION:

APPLICANT: Ramakrishnan, Shyam

TITE OF INVENTION: Regulation of Human Serine Racemase Enzyme

FILE REFERENCE: LIO115-04.

CURRENT APPLICATION NUMBER: US/10/240,466

CURRENT FILING DATE: 2002-09-30

PRIOR PILING DATE: 2000-03-31

PRIOR PLING DATE: 2000-03-31

PRIOR PLING DATE: 2000-04-03

PRIOR APPLICATION NUMBER: US 60/193,748

PRIOR PLING DATE: 2000-04-03

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 340
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Publication No. US20040009491A1

GENERAL INFORMATION:

APPLICANT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PA131P1

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/16450

PRIOR APPLICATION NUMBER: DCT/US01/16450

PRIOR APPLICATION NUMBER: US 60/205,515

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

SOFTWARE PETENTION NUMBER: US 60/205,515

SOFTWARE PETENTION NUMBER: US 60/205,515

LENGTH: 228
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89.4%; Pred. No. 9.2e-146;
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Matches 304; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: II, Fing Title Order of Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With FILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966
                                                                               LOCATION: (209)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
FEATURE:
                                                                                                                                                                                                                             OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids FRATURE:
                                                                                                                                                                                                                                                                                                                         , LOCATION: (2247)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-2089
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89.6%; Pred. No. 3.7e-88;
ive 12; Mismatches 10; Indels
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43.5%; Score 756.5; DB 16; Length
Best Local Similarity 46.6%; Pred. No. 3.3e-65;
Matches 150; Conservative 61; Mismatches 104; Indels
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US-10-437-963-106995
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Barbazuk, Brad
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
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Matches 189; Conservative
                                                                                                                                                                       NAME/KEY: MISC FEATURE LOCATION: (210)
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Homo sapiens
                                                  NAME/KEY: MISC FEATURE
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ORGANISM: Oryza sativa
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Sequence 49567, Application US/10425114
Publication No. US2004003488A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Edou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: NUCLET ACID MOLECULES ASSOCIATED With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
                                                                         125 IVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGOGTIALEVLNQVPLVDALVVPV 184
                                                                                                                    185 GGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSSI 244
                                                                                                                                          245 GLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSP- 303
                                                                                                                                                                                                           253 GDLTWPVVRDLVDDIIVVDDNAIVDAMKMCYEMLKVAVEPSGAIGLAAALSDEFKQSSAW 312
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US-10-425-114-49567
                                                                                                                                                                                                                                                      304 - EVKNVCIVLSGGNVDLTSLNW 324
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Best Local Similarity
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LENGTH: 379
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Sequence 62761, Application US/10425114

Sequence 62761, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Zoren, Steven E

APPLICANT: Tabaska, Jack E

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

SEQUID NOS: 73128

SEQUID NOS: 73128
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Sequence 155663, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21 (53223) B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

LENGTH: 247
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46.7%; Pred. No. 5.8e-54;
tive 55; Mismatches 84; Indels 7;
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OTHER INFORMATION: Clone ID: PAT_MRT3847_111043C.1.pep
US-10-424-599-155063
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US-10-425-114-62761
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Best Local Similarity 46.7%
Matches 128; Conservative
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ORGANISM: Glycine max
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ORGANISM: Zea mays
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SOFTWARE: PatentIn version 3.2
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
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Best Local Similarity 37.7'
Matches 118; Conservative
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244 TL-W 246
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                                                                                                                                                                                            180 SEIIKAMKLCFEILKVVVEPSGAIGLAAVLSDTFOK-NPAWKDCNHIGIVVSGGNVDLAM 238
                                                                                                                                                                     ETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGNVAGIAITIKALKPSV 204
                                                                                                                                                                                                                                                   205 KVYAAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSSIGLNTWPIIRDLVDDVFTVTE 264
                                                                                                                                                                                                                                                                                                                                 265 DEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSP---EVKNVCIVLSGGNVDLTS 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 QETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGMVAGIAITIKALKPS 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 VKVYAAEPSN-ADDCYQSKLKGELTPNLHPPETIADGVKSSIGLNTWPIIRDLVDDVFTV 262
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                                                                                            85 GNHGOALTYAAKLEGIPAYIVVPOTAPNCKKLAIQAYGASIVYCDPSDESREKVTQRIMQ
                                                                                                                              GNHAAALALAAKLRGIPSYIVIPKNAPTCKIENVKRYGGOVVWSEASVQSREEIANKVWQ
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            Length 247;
                                                     Indels
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          Query Match
33.2%; Score 577; DB 15;
Best Local Similarity 44.9%; Pred. No. 8.1e-48;
Matches 109; Conservative 58; Mismatches 70
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LOCATION: (1)..(252)
OTHER INFORMATION: unsure at all Xaa locations
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Matches 104; Conservative
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ORGANISM: Sorghum bicolor
FEATURE:
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APPLICANT: Mourad, George S,
TITLE OF INVENTION: Methods and Compositions for Producing Plants and Microorganisms
TITLE OF INVENTION: that Express Feedback Insensitive Threonine Dehydratase/Deaminase
FILE REFERENCE: PRF-07898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 LIPDIPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 YCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 IHGTVVDETLAAAQEYAAETGAVFIHPFDHPDIIAGQGTVGLEILEQCPEVRTIVVGIGG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 DVPFRIIGDLVDEVRTVSEGNLSSALLLCLERAKLVVEPAGASPVAALLREPGAFEGP-- 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 LNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 ISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVK-SSIG
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                                                                                                                                                                                                                        APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: WASABIIRA
FITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
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Sequence 10839, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 33, Application US/10413943 Publication No. US20040006784A1 GENERAL INFORMATION:
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APPLICANT: Mourad, George S,
TITLE OF INVENTION: Methods and Compositions for Producing Plants and Microorganisms
TITLE OF INVENTION: Methods and Compositions for Producing Plants and Microorganisms
TITLE OF INVENTION: That Express Feedback Insensitive Threonine Dehydratase/Deaminase
FILE REPERENCE: PRF-07898
CURRENT APPLICATION NUMBER: US/10/413,943
CURRENT FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.2
SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 KQLMPQIKVIAVE---AEDSACLKAALEAGHPVDLPRVGLFAEGVAVKRIGDEFFRLCQE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 LVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAV---LSQHFQTVSPEVKNVCIV 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 VVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVYCDPS-DESREK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 VTQRIMQETEGILVHPNOEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGMVAGIAITI 197
       252 IRDLVDDVFTVTEDBIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEV---KNV 308
                                   305 AQQVVDEVVLVNTDEICAAVKDIFEDTRSIVEPSGALSVAG-MKKYISTVHPEIDHTKNT 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 VYEAAQVTPLOKMEKLSSRLDNVILVKREDRÓPVHSFKLRGAYAMMAGL---TEEOKAHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69; Mismatches 127; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
22.1%; Score 384; DB 15;
Best Local Similarity 32.3%; Pred. No. 2e-28;
Matches 102; Conservative 69; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 266101, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             Sequence 31, Application US/10413943 Publication No. US20040006784A1 GENERAL INFORMATION:
                                                                                                         309 CI-VLSGGNVDLTSLNWVGQ 327
                                                                                                                                        ::||| |:: | :| : : 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Salmonella typhimurium US-10-413-943-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312 LSGGNVDLTSLNWVGQ 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 LSGANVNFHGLRYVSE 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-424-599-266101
                                                                                                                                                                                                                                  RESULT 14
US-10-413-943-31
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US-10-413-943-29

Sequence 29, Application US/10413943

Sequence 29, Application No. US20040006784A1

Sequence 29, Application No. US20040006784A1

GENERAL INFORMATION:

APPLICANT: MOUNTED, Methods and Compositions for Producing Plants and Microorganisms TITLE OF INVENTION: that Express Peedback Insensitive Threonine Dehydratase/Deaminas FILE REFERENCE: PRF-07898

FILE REFERENCE: PRF-07898

CURRENT APPLICATION UNMERE: US/10/413,943

CURRENT FILING DATE: 2003-04-15

NUMBER OF SEQ ID NOS: 69

SOFTWARE: Patentin version 3.2

SEQ ID NO 29

LENGTH: 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 KVTQRIMQETEGIL-VHPNQEPAVIAGQGTIALEVLNQVPL---VDALVVPVGGGGMVAG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVK-SSIGLNTWPI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 IGAYLKRVAPHIKTIGVETYDAATLHNSLQRNQRTP-LPVVGTFADGTSVRMIGBETFRV 304
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                                                                                                                                                                                                                                                                                                                               67 LIPDIPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIV 126
                                                                                                                                                                                                                                                                                                                                                                GGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVK-SS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 -YCDPSDESREKVTQRIMQETEG-ILVHPNQEPAVIAGOGTIALEVLNQVPLVDALVVPV 184
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                                                                                                                                                                                                                                     7 ISPADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRG
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                                                                                                                                     27.4%; Score 476; DB 15; I 35.9%; Pred. No. 9.9e-38; ative 70; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 HFQTVSPEVKNVCIVLSGGNVDLTSLNWV 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 NRKTVS-----1ISGGNIDLSRVSQI 323
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ORGANISM: Saccharomyces cerevisiae
US-10-413-943-29
                                                                                                                                             Query Match
Best Local Similarity 35.9
Matches 118; Conservative
                                             TYPE: PRT
ORGANISM: Escherichia coli
                                                                                               US-10-413-943-33
SEQ ID NO 33
LENGTH: 329
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                                                                                                                                                                                                                                                                                                                                                 136 EKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQV--PLVDALVVPVGGGGMVAGI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 AITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETI------ADGVK-SSI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287 AAYVKRVKPEVKIFGVEPTDAN-----AMALSLHHDQRVILDQVGFADGVAVKEV 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 GLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALA---AVLSOHFQTV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 INIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGLIPDTPEEKP 76
                                                                                                                                                           21.8%; Score 380; DB 15; Length 602;
31.8%; Pred. No. 6.4e-28;
tive 65; Mismatches 118; Indels 38; Gaps
; SEQ ID NO 266101
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_8230C.1.pep
US-10-424-599-266101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 SPEVKNVCIVLSGGNVDLTSLNWV 325
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                                                                                                                                                             Query Match 21.8
Best Local Similarity 31.8
Matches 103; Conservative
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Search completed: April 22, 2005, 16:42:20 Job time : 89.3697 secs

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, GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

April 22, 2005, 16:19:29 ; Search time 30.0442 Seconds (without alignments) 844.779 Million cell updates/sec

US-09-889-609B-10 ritle:

Perfect score:

1 MCAQYCISFADVEKAHINIR.....SSITWVKQAERPASYQSVSV 340 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

513545 segs, 74649064 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/cgn2\_6/ptodata/1/iaa/PcTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PcTUS\_COMB.pep:\* Issued Patents AA: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

		de			SUMMAKIES	
Result No.	Score	Query Match	Length DB	DB	ΙD	Description
7	1735	100.0	340	4	US-09-789-300A-2	Sequence 2, Appli
7	601	34.6	332	4	US-09-543-681A-4645	Sequence 4645, Ap
m	578	33.3	328	4	US-09-328-352-4536	Sequence 4536, Ap
4	538	31.0	374	4	US-09-252-991A-31294	
2	457	26.3	524	4	US-09-252-991A-27783	Sequence 27783, A
9	445	25.6	405	4	US-09-902-540-12639	Sequence 12639, A
7	443.5	25.6	411	4	US-09-328-352-5207	Sequence 5207, Ap
80	442	25.5	334	4	US-09-489-039A-14107	Sequence 14107, A
6	403	23.2	677	4	US-09-252-991A-22442	
10	393	22.7	525	4	US-09-543-681A-4364	Sequence 4364, Ap
11	375	21.6	507	4	US-09-424-978B-34	34, Ar
12	369	21.3	521	4	US-09-489-039A-8050	8050
13	367	21.2	424	m	US-09-134-001C-3876	Sequence 3876, Ap
14	367	21.2	424	4	US-09-710-279-1046	
15	355	20.5	518	4	US-09-540-236-3648	Sequence 3648, Ap
16	348.5	20.1	441	Н	US-08-403-866-10	10, Ar
17	344.5	19.9	520	4	US-09-328-352-7451	7451
18	336	19.4	421	4	US-09-107-433-2928	2928,
19	330	19.0	416	4	US-09-583-110-3878	387
20	310.5	17.9	436	m	US-08-669-378-2	2, Api
	310.5	17.9	436	m	US-08-669-378-12	Sequence 12, Appl
22	309.5	17.8	436	m	US-08-669-378-4	4,
23	309.5	17.8	436	ო	US-08-669-378-6	ý
24	309.5	17.8	436	ო	US-08-669-378-10	Sequence 10, Appl
25		17.7	436	ო	US-08-669-378-8	8
26	283.5	16.3	378	4	US-09-789-300A-4	4
27	277.5	16.0	329	4	US-09-843-297-2	7

Sequence 10697, A	Sequence 6763, Ap	Sequence 1, Appli	Sequence 29393, A	Sequence 18227, A	Sequence 4168, Ap	Sequence 29, Appl	Sequence 18228, A	Sequence 4369, Ap	Sequence 4532, Ap	Sequence 3925, Ap	Sequence 17694, A	Sequence 3983, Ap	Sequence 5, Appli	Sequence 161, App	Sequence 1075, Ap	Sequence 2, Appli	Sequence 9, Appli
US-09-949-016-10697	US-09-949-016-6763	US-09-088-435-1	US-09-252-991A-29393	US-09-248-796A-18227	US-09-134-001C-4168	US-09-424-978B-29	US-09-248-796A-18228	US-09-583-110-4369	US-09-107-433-4532	US-09-107-532A-3925	US-09-248-796A-17694	US-09-134-000C-3983	US-09-962-357-5	US-08-311-731A-161	US-09-538-092-1075	US-08-120-960-2	US-09-347-878-9
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347	328	325	331	373	367	392	387	308	317	308	193	225	311	378	550	551	551
15.8	15.3	15.0	14.8	14.0	13.9	13.7	12.2	11.3	11.3	11.2	11.2	11.0	11.0	10.8	10.8	10.8	10.8
274.5	265.5	259.5	256	242.5	241.5	237	211	196.5	196.5	195	193.5	191	190.5	187	187	187	187
88	29	30	31	32	33	34	35	36	37	38	39	9	11	42	<del>1</del> 3	44	5

## ALIGNMENTS

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        Sequence 2, Application US/09789300A
Patent No. 6458576
Patent No. 6458576
Patent No. 6458576
Rachel
APPLICANT: Meyers, Rachel
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: 22406, A No. 6458576el Human Pyridoxal-Phosphate
TITLE OF INVENTION: Dependent Enzyme Family Member and Uses Therefore
FILE REFERENCE: 35800/208926
CURRENT APPLICATION NUMBER: US/09/789,300A
CURRENT APPLICATION NUMBER: US 60/183,208
PRIOR PILING DATE: 2000-02-17
PRIOR PILING DATE: 2000-02-17
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                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                            SEQ ID NO 2
LENGTH: 340
TYPE: PRT
US-09-789-300A-2
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Sequence 31294, Application US/09252991A

Patent No. 651795

Patent No. 651795

Patent No. 651795

Patent No. 651795

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PLILNG DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
                                                  68 VPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVY 127
                                                                          GMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVKSS-IGL 246
                                                                                                                                                                                                                    247 NTWPLIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEV- 305
                                                                                                                                                                                                                                                                                     68 VPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVY 127
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37.7%; Pred. No. 2.5e-52;
Live 67; Mismatches 120; Indels
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Best Local Similarity 37.7%
Matches 118; Conservative
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US-09-252-991A-31294
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US-09-252-991A-31294
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                                        Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON:
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: UNCLEIC AND THERAPEUTICS
TITLE OF INVENTION: UNFORCE: 2709.1002-001
TITLE OF INVENTION: UNFORCE: 105/9543,681A
FILE REFERENCE: 2709.1002-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 33.3%; Score 578; DB 4; Length 328; Best Local Similarity 41.5%; Pred. No. 5.4e-57; Matches 131; Conservative 62; Mismatches 111; Indels
                                     Application US/09543681A
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Patent No. 6562958
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Proteus mirabilis
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310 KIGIIISGGNVDI 322
RESULT 2
US-09-543-681A-4645
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                                 Sequence 4645,
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LENGTH: 328
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; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-12639
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SEQ ID NO 12639
LENGTH: 405
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                                                                                                                             TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27783
LENGTH: 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-27783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 NHGOALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGA-SIVYCEPSDESRENVAKRVTE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETEGIMVHPNQEPAVIAGQGTIALEVLNQVP-LVDALVVPVGGGGMLAGIAITVKALKPS 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 TEDEIKCATOLVWERMKLLIEPTAGVGVAAVLSOHFOTVSPEVKNICIVLSGGNVDL--- 319
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Patent No. 683344710N:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Steven C.
APPLICANT: Hister, Steven C.
APPLICANT: Wiegand, ROGER C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: 02/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 TPVLTSSILNOLTGRNLFFKCELFOKTGSFKIRGALNAVRSLVPDALERKPKAVVTHSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 VKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-SSIGLNTWPIIRDLVDDIFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.3%; Score 457; DB 4; Length 524; llarity 35.2%; Pred. No. 7.8e-43; Conservative 63; Mismatches 127; Indels
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                                                                         Sequence 27783, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity
Matches 116; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: UNSURE LOCATION: (108)
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US-09-902-540-12639
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
SUCHER OF SEQ ID NOS: 8252
LENGTH: 411
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                                                                                                                                                                                                                                                                                       179 GGGGLISGIACALKETRPDIRVVGVQAETIASMKASVEAGERVLLAAAGTTIADGIAVKR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 IGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 ALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIV---- 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 GGGLISGIAIAAKTINPKIKIIGVQSVVYPSMA------KLLCNYQLAVSMGSTVA 236
                                                                                                                                                                                                                                                                                                                                                                        125 IVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPV 184
                                                                                                                          7 ISFADVEKAHINIRDSIHLTPVLTSSILNQLTG-RNLFFKCELFQKTGSFKIRGALNAVR 65
                                                                                                                                                                       15 DIHAAARRIDGLVVKTPFVFSETISKTLGAKOMLKFENLQFTASFKERGALNKLLSL--- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 GGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-SS
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Query Match 25.6%; Score 445; DB 4; Length 405; Best Local Similarity 33.9%; Pred. No. 1.2e-41; Matches 107; Conservative 66; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.6%; Score 443.5; DB 4; Length Best Local Similarity 34.5%; Pred. No. 1.8e-41; Matches 112; Conservative 61; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5207, Application US/09328352 Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Acinetobacter baumannii
US-09-328-352-5207
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297 RGRRTAIILSGGNIDM 312
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Sequence 4364, Application US/09543681A

Patent No. 666779

Patent No. 66779

Patent No. 6779

Patent No. 6
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                                                                                                                                                                                                                                                                                                                                                                                            86 NHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCEPSDESRENVAKRV-TE 144
                                                                                                                                                                                                                                                                                                                                                                                                                          261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 SLVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGA-S 124
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                                                                                                                                                                                                                                                                                                26 TPVLISSILNQLIGRNLFFKCELPOKTGSFKIRGALNAVRSLVPDALERKPKAVVTHSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 ETEGI-MYHPNQEPAVIAGOGTIALEVLNQ-VPLVDALVVPVGGGGMLAGIAITVKALKP
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                                                                                                                                                                                                          23.2%; Score 403; DB 4; Length 67.
33.5%; Pred. No. 1.8e-36;
ive 60; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.7%; Score 393; DB 4; Length 525; 33.0%; Pred. No. 1.6e-35; ive 67; Mismatches 134; Indels
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                                                                                                       TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                         Best Local Similarity 33.55
Matches 111; Conservative
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Best Local Similarity 33.0°
Matches 104; Conservative
                                ; NUMBER OF SEQ ID NOS:
; SEQ ID NO 22442
; LENGTH: 677
                                                                                                                                                     US-09-252-991A-22442
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US-09-543-681A-4364
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                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                     Sequence 14107, Application US/09489039A

Patent No. 6610836

Ratent No. 6610836

RAPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PREMOMORIAE FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: PREMOMORIAE FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/489,039A

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

SEQ ID NO 14107

LENGTH: 334
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Sequence 22442, Application US/09252991A
Patent No. 6551795
GENERAL INPRMATION:
PAPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
CURRENT APPLICATION NUMBER: US/092.291A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
DGVK-SSIGLNIWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQ 296
                              67 LVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKIAIQAYGASIV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 YCEPSDESRENVAKR--VTEFTEGIMVHPNQEPAVIAGOGTIALEVLNQVPLVDALVVPV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 L--HGDNFNDTLAKASDIVELEGRIFIPPYDDPQVIAGGGTIGLEILEDLYDVDNVIVPI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 ISFADVEKAHINIRDSIHLIPVLISSILNQLIGRNLFFKCELFQKIGSFKIRGALNAVRS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 GGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-SS 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 VSIDDILEAKQRLAGKIYKTGMPRSNYFSERCQGEIFLKFENMQRTGSFKIRGAFNKLCG 73
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; Pred. No. 1.9e-41;
66; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 HFQTVSPEVKNICIVLSGGNVDLT--SSIT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.5%; Score 442; 34.8%; Pred. No. 1
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-----PDLFLGHKVGVVLSGGNID 315
                                                                                           297 HFQTVSPEV---KNICIVLSGGNVD 318
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ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Best Local Similarity
Matches 115; Conserv
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US-09-252-991A-22442
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244 IGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 DALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 DALAR---GVITASAGNHAQGVAFSAARMGVKAVIVVPVTTPQVKVDAVRAHGGFGVEVI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-SS 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 QAGESYSDAYAHALKVQEERGLTFVHPFDDPYVIAGQGTIAMEILRQHQGP-IHAIFVPI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 IGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSP 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.6%; Score 375; DB 4; Length 50
33.3%; Pred. No. 1.7e-33;
ive 59; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kinney, Anthony J.
APPLICANT: Abell, Lynne N.
APPLICANT: Thorpe, Catherine J.
TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: BB-1087
CURRENT APPLICATION NUMBER: US/09/424,978B
CURRENT FILING DATE: 1999-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/048,771
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 34
LENGTH: 507
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; Sequence 8050, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
                                                                                                                                                                                                                                     Sequence 34, Application US/09424978B Patent No. 6664445
                                                                                                                                                                                                                                                                                      APPLICANT: Falco, Saverio Carl
APPLICANT: Allen, Seephen M.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Hitz, William D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Burkholderia capacia
                                                                                                                    304 EVKNICIVLSGGNVD 318
                                                                                                                                         307 KGERLAHVLSGANVN 321
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Best Local Similarity 33.39
Matches 105; Conservative
                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                       US-09-424-978B-34
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE DE INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE DE INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 QLMPQIKVIAVE---AEDSACLKAALDAGHPVDLPRVGLFAEGVAVKRIGDETFRLCQEY 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 AKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGMLAGIAITVK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 AIELAQQQGFTWVPPFDHPMVIAGQGTLALELLQQDAHIDRVFVVGGGGLAAGVAVLIK 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 ALKPSVKVYAAEPSNADD--CYQSKLKGKLMPNLYPPETIADGVK-SSIGLNTWPIIRDL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 VDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAV---LSQHFQTVSPEVKNICIVL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 IRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDALERKPKA
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                                                                                                                                                                                                                                                                                                                                                              Length 521;
                                                                                                                                                                                                                                                                                                                                                                                                                64; Mismatches 129; Indels
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                                                                                                                                                                                                                                                                                                                                                              21.3%; Score 369; DB 4; 31.7%; Pred. No. 8.6e-33;
TITLE OF INVENTION: NUCLEIC ACID AND AMINO A
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTI
FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT PILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3876, Application US/09134001C
Patent No. 6380370
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US-09-134-001C-3876
                                                                                                                                                                                                                                                                                   Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                97; Conservative
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Best Local Similarity
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Best Local Similarity
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US-09-134-001C-3876
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ORGANISM:
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Mon Apr 25 11:37:07 2005

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125 -IVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGOGTIALEVINOV----PLVDA 179
67 LVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGAS-- 124
                                                                       126 BIVLIGDIFDHCLAQALAYTKQHGANFIDPFNNVYTIAGQGTLAKEIINQAEKEDKTFDY 185
                                                                                                        180 LVVPVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADG 239
                                                                                                                          240 VK-SSIGLNTWPIIRDLVDDIFTVTEDBIKCATQL-VWERMKLLIEPTAGVGVAAVLSQH 297
                                                                                                                                                                               246 ASVARVGDITFDIAKDKVDDYVQVDEGAV-CSTILDMYSKQAIVAEPAGALSVSA-LEQY 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 -IVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGOGTIALEVLNQV----PLVDA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 LVVPVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKIKGKLMPNLYPPETIADG 239
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9 VSTKDIDEAYLRLKNIVKETPLQFDHYLSQKYNCNVYLKREDLQWVRSFKLRGAYNAISV 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 21.2%; Score 367; DB 4; Length 424; Best Local Similarity 31.1%; Pred. No. 1e-32; Matches 100; Conservative 64; Mismatches 142; Indels
                                                                                                                                                                                                                  298 FQTVSPEVKNICIVLSGGNVDL 319
                                                                                                                                                                                                                                     304 KKQI--ENKTIVCIVSGGNNDI 323
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ORGANISM: Artificial Sequence
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Sequence 3648, Application US/09540236

Batent No. 6673910

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARFILLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT APPLICATION NUMBER: US/09/540,236

NUMBER OF SEQ ID NOS: 3840

LENGHAL SIS
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                                                                                                                                                                                                                                                                                                                                                                                                   23 AIH-TPLEPATKLSKKFDNHIRLKREDLQPVFSFKLRGAYNKI-SQLSDA--QKQKGIIC 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 LKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGYK-SSIGLNTWPIIR----
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                                                                                                                                                                                                                                                                                                           20.5%; Score 355; DB 4; Length 518; 32.4%; Pred. No. 3.4e-31; ive 63; Mismatches 126; Indels
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Job time : 31.0442 secs
                                                                                                                                                                                                                                                                                                                        Local Similarity 32.4
nes 100; Conservative
                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: M.catarrhalis
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RESULT 15
US-09-540-236-3648
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US-09-540-236-3648
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Matches
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Sequence 106995,
Sequence 49567, A
Sequence 62761, A
Sequence 43071, A
Sequence 10839, A
Sequence 33, Appl
Sequence 33, Appl
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Sequence 2, Appli
Sequence 2, Appli
                                                                                                                                                  April 22, 2005, 16:23:43 ; Search time 88.6303 Seconds (without alignments) 1276.639 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                            1 MCAQYCISFADVEKAHINIR......SSITWVKQAERPASYQSVSV 340
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| cgn2 6/ptodata/1/pubpaa/PCT PUBCOMB.pep:*
| cgn2 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*
| cgn2 6/ptodata/1/pubpaa/USOP PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-240-800-2
US-10-240-466-2
US-10-240-466-2
US-10-264-237-2089
US-10-437-963-106995
US-10-425-114-49567
US-10-425-114-49567
US-10-424-599-155063
US-10-767-701-43071
US-10-156-761-10839
US-10-413-943-33
US-10-425-114-39197
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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-10-425-114-55647 -10-413-943-29 -10-424-599-26610 -10-425-114-38570	-10-437-963-1388 -10-413-943-8 -10-413-943-12 -10-413-943-10	413-943-8 413-943-4 413-943-6 413-943-6 413-943-6 413-943-6	10-413-943- 10-413-943- 10-413-943- 10-413-943- 10-413-943- 10-713-928- 10-77-701-	-626-582 7-226-67 -300A-4 -966-4 7-072-17 7-072-17 7-71-43
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61 INAVRSLVPDALERKPKAVVTHSSGNHGQALTYAARKLEGIPAYIVVPQTAPDCKKLAIQA 120
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                                                                                                           APPLICANT: Meyers, Rachel
APPLICANT: Meyers, Rachel
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: 22406, A No. 6458576el Human Pyridoxal-Phosphate
TITLE OF INVENTION: 22406, A No. 6458576el Human Pyridoxal-Phosphate
TITLE OF INVENTION: Dependent Enzyme Family Member and Uses Therefore
FILE REFERENCE: 35800/208926
FILE REFERENCE: 35800/208926
CURRENT APPLICATION NUMBER: US/09/789, 300A
CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: US 60/183, 208
PRIOR FILING DATE: 2000-02-17
NUMBER OF SEO ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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                   Sequence 2, Application US/09789300A
Publication No. US20020115137A1
GENERAL INFORMATION:
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US-09-789-300A-2
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LENGTH: 340
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                                                                                                                    MCAQYCISFADVBKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGA
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100.0%; Pred. No. 2.4e-162;
iive 0; Mismatches 0;
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Publication No US20030212262A1
GENERAL INPORMATION:
FILE OF INVENTION: HUMAN SERINE RACEMASE
FILE REFERENCE: 20642Y-PCT
CURRENT PELING DATE: 2002-10-03
PRIOR FILING DATE: 2002-10-03
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 340, Conservative
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US-10-240-800-2
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US-10-240-800-2
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LENGTH: 340
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                      VVPVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGV
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                                                                                                       VSPEVKNICIVLSGGNVDLTSSITWVKQAERPASYQSVSV 340
                                                                                                                   301 VSPEVKNICIVLSGGNVDLTSSITWVKQAERPASYQSVSV 340
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Sequence 2, Application US/10164966
Publication No. US20030064439A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Matches 152;
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ORGANISM:
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; Sequence 2089, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
    TITLE OF INFORMATION:
    TITLE OF INFORMATION:
    FILE REFREENCE: PA131P1
; CURRENT FILING DATE: 2002-10-04
; PRIOR PAPLICATION NUMBER: PCT/US01/16450
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2000-05-18
; PRIOR FILING DATE: 2000-05-18
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PATENTIN VET. 3.1
; SEQ ID NO 2089
LENGTH: 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 99.8%; Score 1731; DB 14; Length 340; Best Local Similarity 99.7%; Pred. No. 6e-162; Matches 339; Conservative 1; Mismatches 0; Indels 0
                                        5-10-240-466-2
Sequence 2, Application US/10240466
Sequence 2, Application US/10240466
Publication No. US20030175941A1
GENERAL INFORMATION:
APPLICANT: Ramakrishnan, Shyam
TITLE OF INVENTION: Regulation of Human Serine Racemage Enzyme FIER REFERENCE: LIO115-US
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PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US 60/193,748
PRIOR RILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 2
SOFWARE: Patentin version 3.0
SEQ ID NO 2
                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/240,466 CURRENT FILING DATE: 2002-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-10-240-466-2
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Associated With
                                                                          LOCATION: (209)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (2247)

OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-2089
                                                                                                                                                                                                        OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(33221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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                                                                                                                                                                                                                                                                                                                                                                                          Score 1062.5; DB 15; Lengt
Pred. No. 3.3e-96;
2; Mismatches 12; Indels
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US-10-437-963-106995
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47.1%; Pred. No. 1.8e-67;
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Publication No. US20040123343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 93.4%;
Matches 213; Conservative
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                                                                                                                           PEATURE:
NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Oryza sativa
Homo sapiens
                                                 NAME/KEY: MISC_FEATURE
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Best Local Similarity
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Sequence 62761, Application US/10425114

Publication No. US20040034888A1

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Good Secondary

APPLICANT: Application Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT APPLICATION NUMBER: US/10/425,114

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 62261

LENGTH. 200
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEG ID NOS: 285684
SEQ ID NO 155063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 GSFKIRGALNAVRSIVPDALERKPKAVVTHSSGNHGGALTYAAKLEGIPAYIVVPOTAPD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 CKKLAIQAYGASIVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGGGTIALEVLN 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 OVPLVDALVVPVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 PETIADGVKSSIGLNTWPIIRDLVDDIFTVTEDEIKCATOLVWERWKLLIEPTAGVGVAA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.5%; Score 651; DB 15; Length 280;
47.6%; Pred. No. 1.9e-55;
tive 56; Mismatches 79; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT3847_111043C.1.pep
US-10-424-599-155063
                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: LIB3591-097-G1_FLI.pep
US-10-425-114-62761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 VLSQHFQTVSP--EVKNICIVLSGGNVDL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 ALSDEFKQSSAWHESSKIGIIVSGGNVDL 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 155063, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
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Best Local S
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Soreal, Steven E
APPLICANT: Soreal, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cac, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21 (53313)8
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 49567
LENGTH: 379
125 IVYCEPSDESRENVAKRVTEFTEGIMVHPNQEPAVIAGGGTIALEVLNQVPLVDALVVPV 184
                                                                                                                     185 GGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVKSSI 244
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253 GDLTWPUVRDLVDDIIVVDDNAIVDAMKMCXEMLKVAVEPSGAIGLAAALSDEFKQSSAW 312
                                                                                                                                                                                     245 GLNTWPIIRDLVDDIFTVTEDEIKCATOLVWERMKLLIEPTAGVGVAAVLSOHFOTVSP- 303
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| S7 YAADIDSIREAQARIAPYVHRTPVMSSTSIDAMVGKKLFFKCECEGKAGAFKIRGASNSI 116
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117 FALDD---EQVSKGVVTHSSGNHAAAVALAAKLRGIPAHIVIPRNAPACKVENVKRYGGH 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 GGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVKSSI 244
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|234 SGGGLISGVALAAKAINPSIRILAAEPKGADDSAQSKAAGKII-TLPSTNTIADGLRAFL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 GINTWPIIRDLYDDIFTYTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSP- 303
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46.1%; Pred. No. 1.6e-65;
tive 66; Mismatches 99; Indels
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US-10-425-114-49567
                                                                                                                                                                                                                                                    304 -EVKNICIVLSGGNVDLTSSITW 325
                                                                                                                                                                                                                                                                            313 HESSKIGIIVSGGNVDL--GVLW 333
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Publication No. US20040034888A1
GENERAL INFORMATION:
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HESSKIGIIVSGGNVDL 369
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Best Local Similarity
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ORGANISM: Zea mays
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APPLICANT: Mourad, George S,
TITLE OF INVENTION: Methods and Compositions for Producing Plants and Microorganisms
TITLE OF INVENTION: that Express Peedback Insensitive Threonine Dehydratase/Deaminase
TITLE OF INVENTION: that Express Peedback Insensitive Threonine Dehydratase/Deaminase
FILE REFERENCE: PRF-07898
CURRENT APPLICATION NUMBER: US/10/413,943
CURRENT FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.2
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 LVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASI- 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 VYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVG 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 GGGLAAGIATAVKALRPDVRIVGVQAAGA-AAYPPSLAAGRPVSVENPATMADGIKVGRP 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 ISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.6%; Score 479.5; DB 14; Length
37.9%; Pred. No. 2.8e-38;
tive 53; Mismatches 131; Indels
                                                                                                                                                                                                                                         APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
SEQ ID NO 10839
                         Sequence 10839, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Streptomyces avermitilis US-10-156-761-10839
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. Sequence 33. Application US/10413943
. Publication No. US20040006784A1
. GENERAL INFORMATION:
                                                                                                                                     IKEDA, HARUO
ISHIKAWA, JUN
HORIKAWA, HIROSHI
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Matches 119; Conservative
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                                                                                                            APPLICANT: OMURA, SATOSHI
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 43071
                                                                                                                                                                                                                                                     180 SEIIKAMKLCFEILKVVVEPSGAIGLAAVLSDTPQK-NPAWKDCNHIGIVVSGGNVDL-- 236
                                                                                                            85 GNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCEPSDESRENVAKRVTE 144
                                                                                                                                                                                                                     ETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGMLAGIAITVKALKPSV 204
                                                                                                                                                                                                                                                                                                                               205 KVYAAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVKSSIGLNTWPIIRDLVDDIFTVTE 264
                                                                                                                                                                                                                                                                                                                                                                                  121 RIFAAEPKGADDAAQSKAAGRII-RLPETNTIADGLRAFLGDFTWPVVRDLVEEIITVED 179
                                                                                                                                                                                                                                                                                                                                                                                                                                           DEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSP---EVKNICIVLSGGNVDLTS 321
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     DB 15; Length 247;
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43.9%; Pred. No. 3.4e-42;
Live 48; Mismatches 82; Indels
                                                        65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: SORBI-28MAY03-C9309_1.pep
Query Match 34.0%; Score 590.5; DB 19 Best Local Similarity 46.3%; Pred. No. 1.4e-49; Matches 113; Conservative 59; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
LOCATION: (1)..(252)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 43071, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
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Best Local Similarity 43.9%
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :: |
237 AMLW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 SITW 325
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Sequence 29, Application US/10413943
Publication No. US20040006784A1
GENERAL INFORMATION:
APPLICANT: Mourad, George S,
TITLE OF INVENTION: Methods and Compositions for Producing Plants and Microorganisms
TITLE OF INVENTION: Methods and Compositions for Producing Plants and Microorganisms
FILE REFERENCE: PRF-07898
CURRENT APPLICATION NUMBER: US/10/413,943
CURRENT FILING DATE: 2003-04-15
                                                                                                                                                                                                                                                                APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack B
APPLICANT: Tabaska, Jack B
APPLICANT: Tabaska, Jack B
APPLICANT: Tabaska, Jack B
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)8
FILE REFERENCE: 38-21(53313)8
CURRENT APPLICATION WUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                    70 DALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 GMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-SSIGL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 NTWPLIRDLVDDIFTVTEDBIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEVK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 HLTPVLTSSI-----LNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|| ||:|:
9 YLTSVLSSKVYDVAIESPLQLASKLSHRLGVNIWIKREDLQPVFSFKLRGAVNMAKLSR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 TEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEVKNICIVLSGGNVD 318
                                                                                                    130 PSDESRENVAKRVTEETEGIMVHPNOEPAVIAGOGTIALEVLNOV--PLVDALVVPVGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 22.3%; Score 387.5; DB 15; Best Local Similarity 32.4%; Pred. No. 4.8e-29; Matches 101; Conservative 65; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: 700478009_FLI.pep US-10-425-114-55647
                                                                                                                                                                                                            ; Sequence 55647, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION:
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                                                                                                                                                                                            US-10-425-114-55647
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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack B
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 39197
                                                                                                                                                                                      67 LVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIV 126
                                                                                                                                                                                                                69 LT-DA--EKRKGVVACSAGNHAQGVSLSCAMLGIDGKVVMPKGAPKSKVAATCDYSAEVV 125
                                                                                                                                                                                                                                                                                      127 YCEPSDESRENVAKRVTE--ETEG-IMVHPNQEPAVIAGOGTIALEVINQVPLVDALVVP 183
                                                                                                                                                                                                                                                                                                                                        184 VGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-S 242
                                                                                                                                                                                                                                                                                                                                                              243 SIGLNIWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLS----- 295
                                                                                                                                      242 RPGNLTYELVRELVDDIVLVSEDEIRNSMIALIQRNKVVTEGAGALACAALLSGKLDQYI 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 TEGIMVHPNQEPAVIAGQGTIALEVLNQV--PLVDALVVPVQGGGMLAGIAITVKALKPS 203
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                                                                                          Gaps
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                                      26.3%; Score 457; DB 15; Length 329; 36.6%; Pred. No. 3.4e-36; Live 65; Mismatches 117; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 22.4%; Score 388.5; DB 15; Length 499; Best Local Similarity 33.4%; Pred. No. 3.7e-29; Matches 99; Conservative 64; Mismatches 124; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OHFOTVSPEVKNICIVLSGGNVDLT--SSIT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: 700350418_FLI.pep
US-10-425-114-39197
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Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                  Query Match 26.3
Best Local Similarity 36.6
Matches 121; Conservative
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ORGANISM: Zea mays
US-10-413-943-33
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78 AVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIV-YCEPSDESRE 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 QQVVDEVVLVNTDEICAAVKDIFEDTRSIVEPSGALSVAG-MKKYISTVHPEIDHTKNTY 364
                                                                                                                                                                                                                     18 NIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDALERKPK 77
                                                                                                                                                Query Match 22.3%; Score 387.5; DB 15; Length 576; Best Local Similarity 33.9%; Pred. No. 5.7e-29; Matches 105; Conservative 59; Mismatches 131; Indels 15; Gaps
                                                                      TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-413-943-29
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.2
SEQ ID NO 29
LENGTH: 576
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365 VPILSGANMN 374
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